

Optimised Misalignment Correction from Cine MR Slices using Statistical Shape Model

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Abstract. Cardiac magnetic resonance (CMR) imaging is a valuable imaging technique for the diagnosis and characterisation of cardiovascular diseases. In clinical practice, it is commonly acquired as a collection of separated and independent 2D image planes, limiting its accuracy in 3D analysis. One of the major issues for 3D reconstruction of human heart surfaces from CMR slices is the misalignment between heart slices, often arising from breathing or subject motion. In this regard, the objective of this work is to develop a method for optimal correction of slice misalignments using a statistical shape model (SSM), for accurate 3D modelling of the heart. After extracting the heart contours from 2D cine slices, we perform initial misalignment corrections using the image intensities and the heart contours. Next, our proposed misalignment correction is performed by first optimally fitting an SSM to the sparse heart contours in 3D space and then optimally aligning the heart slices on the SSM, accounting for both in-plane and out-of-plane misalignments. The performance of the proposed approach is evaluated on a cohort of 20 subjects selected from the UK Biobank study, demonstrating an average reduction of misalignment artifacts from 1.14 ± 0.23 mm to 0.72 ± 0.11 mm, in terms of distance from the final reconstructed 3D mesh.

Keywords: Cardiac mesh reconstruction · Cine MRI · Misalignment correction · Statistical shape model.

1 Introduction

Cardiac magnetic resonance (CMR) imaging is a noninvasive imaging modality for obtaining functional and anatomical information of the heart. Because of its ability to characterise soft tissues, CMR is increasingly used to evaluate the myocardium, providing accurate assessments of left ventricular (LV) function, myocardial perfusion, oedema, and scar [3]. Clinically used cine MR studies acquire only a small number of image planes with good contrast between soft

tissues at a reasonable temporal resolution, with an about $1.5 \times 1.5 \text{ mm}^2$ in-plane resolution and 8–10 mm out-of-plane resolution. Although 2D CMR images can exhibit the presence of scar or oedema, or myocardial perfusion on heart structures, their visualisation on the 3D heart shape can help in the understanding of their locations and shapes. Heart shape has been shown to improve diagnosis and prediction of patient outcome, which necessitate the development of patient-specific 3D anatomical models of the human heart from CMR images.

The 3D heart mesh reconstruction from cine MR slices is usually affected by several artifacts, specifically the breathing artifact from each plane being acquired at separate breath-holds, and the data sparsity from limited number of image slices. Although significant research has been performed for reconstructing 3D surfaces from 2D images [4], a limited number of methods has attempted this problem for 3D heart meshes, specifically from sparse 2D cine MR slices. In order to compensate for the slice misalignment, some methods used slice-to-volume registration [5, 12], while a geometry-based approach for smoothing epicardial shape using iterative application of in-plane translations was developed in [9]. One of the most common approaches for misalignment correction in heart slices is slice-to-slice registration. Villard et al. [11] optimised the similarity between intensities at the intersecting line between cine MR slices to achieve optimal consistency between cross sectional intensity profiles. Some methods preferred to use a fixed slice, usually long axis (LAX) slice, as a reference plane to align other slices [7].

Although there exist few research works that addressed the problem of misalignment correction from cine MR slices, most of them relied upon the consistency between sparse heart slices in 3D space and hence, could reliably account for only in-plane slice misalignments. In this regard, the objective of the current work is develop a method to optimally correct for slice misalignment, both in-plane and out-of-plane, for accurate patient-specific modelling of the heart surfaces. After extracting the heart contours, namely, LV and right ventricle (RV) endocardium and LV epicardium, we have first performed initial misalignment corrections, first using the image intensities and next using the heart contours, when both LAX and short axis (SAX) cine MR slices are available. In order to perform the optimised misalignment correction, we have first optimally fitted a statistical shape model (SSM) on the sparse heart contours in 3D space and then optimally aligned the heart slices on the SSM, accounting for both in-plane and out-of-plane movements. The performance of the proposed approach is evaluated by reconstructing biventricular heart surfaces from the optimally aligned cine MR slices using a surface generating algorithm [10]. On a cohort of 20 subjects randomly selected from the UK Biobank study [8], the proposed approach has been able to reduce the average misalignment from $1.14 \pm 0.23 \text{ mm}$ to $0.72 \pm 0.11 \text{ mm}$, over the final reconstructed surface meshes.

2 Preprocessing and Initial Misalignment Corrections

2.1 Preprocessing

The MR slices for the standard cine MRI protocol are horizontal long axis (HLA) or 4 chamber view (Fig. 1, column 1), vertical long axis (VLA) or 2 chamber view (Fig. 1, column 2), left ventricular outflow tract (LVOT) or 3 chamber view (Fig. 1, column 3), and the stack of SAX views (Fig. 1, columns 4-5). In order to identify the epicardial contours and LV and RV endocardial contours from all cine MR slices, we have automatically segmented the heart slices in 4 classes, namely, LV cavity, LV myocardium, RV cavity, and background. We have employed the deep learning based method proposed by Bai et al. [2] for this step, since it has been shown to segment heart structures from cine MR slices with human-level accuracy. Since at this time we do not have any pre-trained network for the VLA and LVOT slices, we have manually contoured the LV and RV endocardial and LV epicardial surfaces on the LVOT slices and LV endocardial and epicardial surfaces on the VLA slices. Following segmentation, the heart contours are identified as the boundaries of segmented regions. The septal wall is identified as the intersection between LV epicardium and RV endocardium. An example of the input cine LAX and SAX slices with misalignment artifact is presented in the first row of Fig. 1. In Fig. 1, the HLA, VLA, and LVOT slices in first three columns have been annotated with red, green, and cyan colours, respectively; while the SAX slices in last two columns are annotated with yellow. The relative position of each slice is provided on all of the other slices. The HLA, VLA, and LVOT slices are presented with red, green, and cyan colours, respectively, on both SAX slices, while both SAX slices are presented as yellow lines over all three LAX slices.

2.2 Intensity and Contours Based Misalignment Corrections

In case both LAX and SAX cine MR slices are available, we have performed an initial misalignment correction based on intensity profiles [11]. The objective of this step is to provide spatial consistency to the slices in 3D space by comparing the intensity profiles at the line formed by the intersection between two slices. We have minimised the global motion discrepancy, defined as the sum of dissimilarity measures (here, normalised cross correlation) between a pair of intersecting slices, by estimating the optimal rigid transformation for each slice. We have adopted an iterative minimisation of partial terms, where, in each iteration, the rigid transformation for each slice is sequentially optimised, keeping others fixed.

Using the extracted heart contours, an iterative misalignment correction algorithm is next applied, in order to achieve in-plane alignment of LAX and SAX contours. The Euclidean distance between LAX and SAX contours is used as the dissimilarity measure in global motion discrepancy. A qualitative result of contours based misalignment correction on 2D cine MR slices is presented in second row of Fig. 1, while the sparse 3D representation of the same heart contours after misalignment correction is shown in first column of Fig. 2.

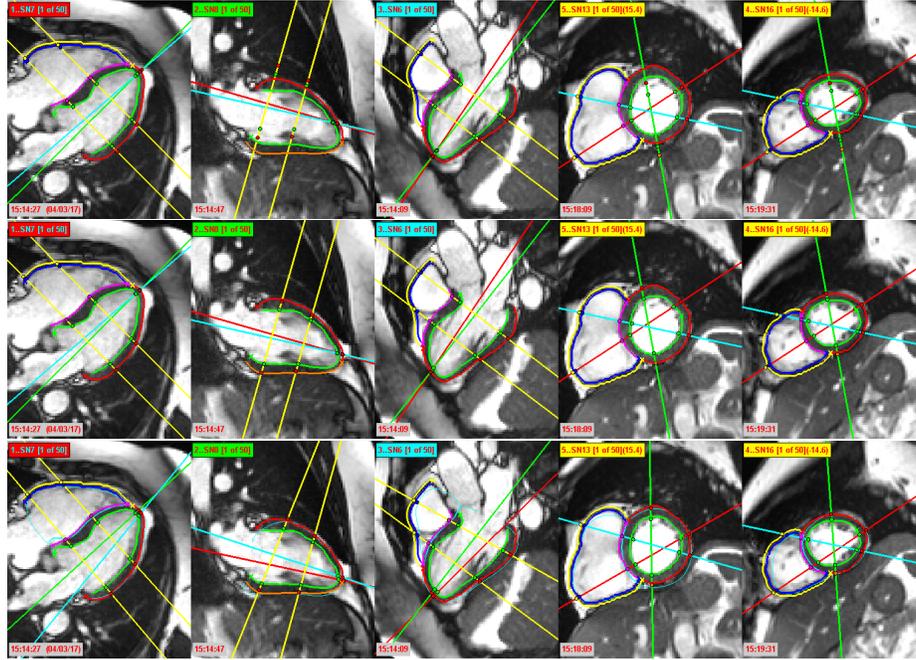


Fig. 1. From left to right: HLA view, VLA view, LVOT view, and two SAX slices. From top to bottom: the misaligned cine MR slices; after contours based misalignment correction; and after SSM based misalignment correction. The green, blue, red, yellow, and pink contours respectively denote the LV and RV endocardial contours, LV and RV epicardial contours, and the septal wall on 2D cine MR slices. The coloured dots represent the position of corresponding contours on the intersecting slice.

3 Proposed Misalignment Correction Using Statistical Shape Model

Our proposed approach of misalignment correction consists of two steps: fitting a statistical shape model (SSM) to the sparse heart contours in 3D space and then optimally aligning the heart slices to the fitted SSM.

3.1 Fitting the Statistical Shape Model

The optimum misalignment correction based only on the intensity profiles or the intersections between sparse LAX and SAX slices is an ill-posed problem and hence, can produce undesirable solutions if out-of-plane transformations are considered. Hence, the global motion discrepancy for both intensity and contours based misalignment corrections is optimised over only the in-plane rigid transformations. Now, although it can significantly reduce the misalignments, one major cause of misalignment, the motion artifacts between image acquisitions, cause

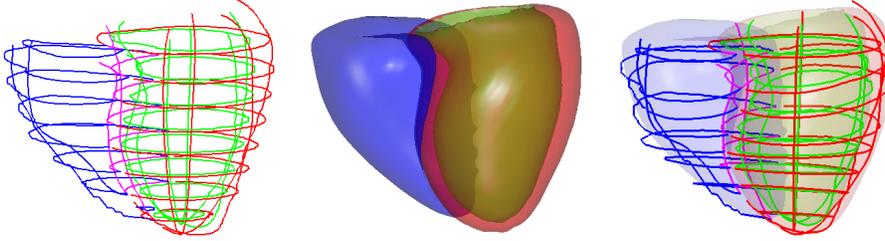


Fig. 2. (a) Sparse 3D contours after contours based misalignment correction; (b) the fitted SSM; and (c) the optimal misalignment corrected heart contours on fitted SSM.

out-of-plane movements. Here, the in-plane rigid transformation is defined as the rigid transformation (translation and rotation) of the cine MR slice along the original acquisition plane; while the out-of-plane rigid transformation can consider rigid transformation outside the acquisition plane for optimal correction of the misalignment artifacts.

In order to estimate the optimal rigid transformations of the cine slices in 3D space for accurate surface reconstruction, we have employed a statistical shape model of human heart ventricles by Bai et al. [1, 6]. The SSM was created by registering 1093 hearts, generated by high-resolution 3D cine MR images, to the template space using rigid registration, thus removing the position and orientation differences, and then by applying the principal component analysis on the surface meshes of LV, RV, and both ventricles. The first 100 principal components, accounting for 99.9% of the total shape variation in the dataset, and the mean SSM are publicly available at <http://wp.doc.ic.ac.uk/wbai/data/>.

For our proposed misalignment correction, we have first extracted the LV and RV endocardial and LV epicardial surfaces from the shapes of LV, RV, and both ventricles of the model. The surface meshes from the model are then fitted to the sparse heart contours in 3D space by the optimal estimation of the 100 principal components of the SSM, followed by rigid transformation. The optimally fitted SSM over the sparse heart contours of Fig. 2(a) is presented in Fig. 2(b). The green, blue, and red surfaces in Fig. 2(b) respectively denote the LV and RV endocardial and LV epicardial surfaces in the fitted SSM.

3.2 Misalignment Correction Using the SSM

Since the SSM was generated from high-resolution 3D cine MR images, there is no misalignment artifact present in this model. Hence, the main objective of obtaining the fitted SSM is to provide a reference for the alignment of heart contours from the cine slices. In order to optimally remove the misalignment artifacts, here we have applied both in-plane and out-of-plane 3D rigid transformations, i.e. translation t_i and rotation R_i for each slice i , to optimally align the heart contours on cine MR slices to the fitted SSM. Along with accounting

for out-of-plane misalignments, another major advantage in the proposed SSM based misalignment correction approach is that it can be applied even in the absence of any LAX slices, which would make both intensity based and contours based misalignment corrections inoperable. An example of the performance of proposed misalignment correction using the fitted SSM on 2D cine MR slices is presented in the third row of Fig. 1, while the same misalignment corrected heart contours on fitted SSM in 3D space is presented in Fig. 2(c). In this regard, it should be noted that the sole objective of the SSM is for guiding a robust misalignment correction of the heart contours. Hence, after the misalignment correction step, the fitted shape model is discarded, and only the aligned heart contours are used for 3D heart surface reconstruction.

After the final alignment of heart contours, the 3D surface meshes are generated, for both qualitative and quantitative evaluations, from each of the LV and RV endocardiums and the epicardium. We have applied the method proposed by Villard et al. [10], that can generate 3D surface mesh from sparse, heterogeneous, non-parallel, cross-sectional, non-coincidental contours. The algorithm applies a composition of smooth deformations aiming at maximising fitting to image contours, thus ensuring a good matching of the reconstructed 3D biventricular surface to the input data, as well as optimal interpolation characteristics.

4 Experimental Analysis

In order to evaluate the reconstruction performance of the proposed misalignment correction approach, we have randomly selected a cohort of 20 subjects from the UK Biobank study [8]. The dataset includes an HLA, a VLA, an LVOT, and a stack of SAX cine MR slices for each subject. The number of SAX cardiac cine MR slices varies between 8 to 13, while the number of acquired frames over a cardiac cycle is 50. The images have in-plane resolution of 1.8269 mm and the distance between SAX slices is 10 mm. For each subject, the frame number 1 is selected as the end-diastolic frame in our analysis.

The qualitative performance of the 3D biventricular surface mesh reconstruction over misaligned slices and after intensity based, contours based, and SSM based misalignment corrections are respectively presented in columns of Fig. 3. Over each reconstructed surface, the distances between sparse heart contours and the reconstructed surface are shown using a continuous color scale varying between 0-5 mm. The quantitative analysis is presented in Fig. 4 using box-plots, by computing the distances of LV endocardial, RV endocardial, and epicardial contours from the reconstructed LV endocardium, RV endocardium, and epicardium, respectively.

In our dataset of 20 subjects, the initial misalignment between the heart contours, measured with respect to the reconstructed heart surfaces, was average 0.98 ± 0.30 mm for the LV endocardial contours, average 1.14 ± 0.22 mm for the RV endocardial contours, and average 1.22 ± 0.26 mm for the epicardial contours. From the quantitative results presented in Fig. 4, it can be observed that the intensity based misalignment correction method has been able to significantly

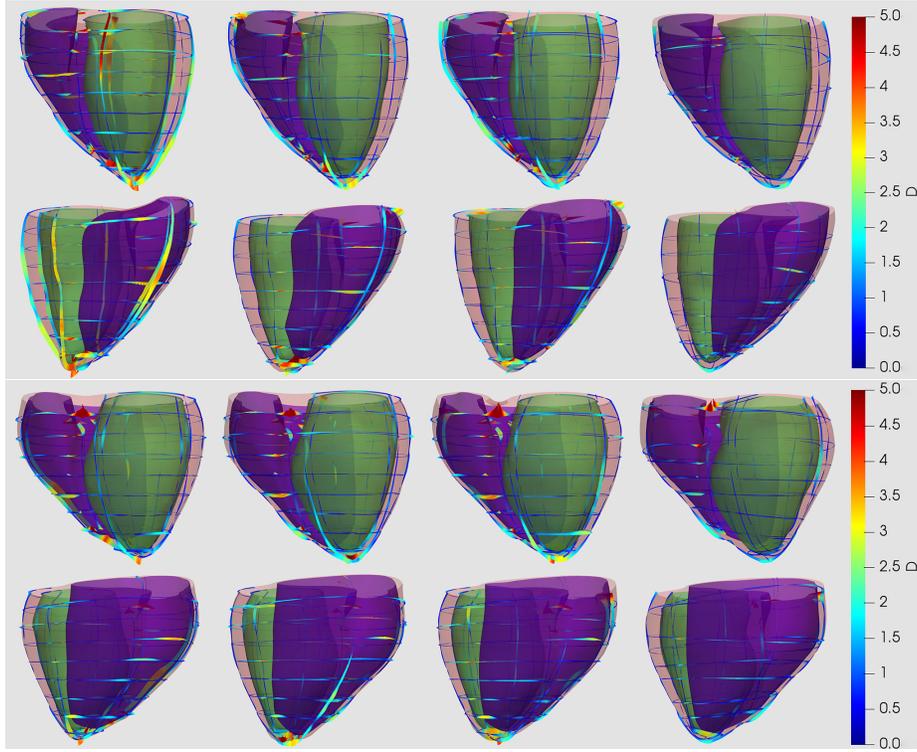


Fig. 3. From left to right: the reconstructed 3D heart surfaces from misaligned heart slices, after intensity based misalignment correction, after contours based misalignment correction, and after SSM based misalignment correction. Top: the anterior view; bottom: the posterior view. Over each reconstructed surface, the distances between heart contours and the surface are shown using a continuous color scale varying between 0-5 mm (defined at the right margin). The green, blue, and red surfaces respectively denote the LV and RV endocardium and the epicardium.

reduce the misalignment of heart contours to average 0.72 ± 0.14 mm for LV endocardial contours, average 1.04 ± 0.17 mm for RV endocardial contours, and average 1.04 ± 0.19 mm for epicardial contours. In most cases, the results are also statistically significant with respect to the parametric paired- t test, where 0.05 is the desired level of significance. On the other hand, the contours based misalignment correction method has been able to reduce the misalignment error to average 0.64 ± 0.11 mm for LV endocardial contours, average 0.82 ± 0.12 mm for RV endocardial contours, and average 0.94 ± 0.17 mm for epicardial contours.

From the quantitative results presented in Fig. 4 and in Fig. 3, it is clearly observed that the proposed SSM based misalignment correction method has been able to significantly reduce the misalignment artifacts from cine MR slices for all subjects below sub-voxel accuracy. After the proposed misalignment correction, the average misalignment errors for LV endocardial, RV endocardial,

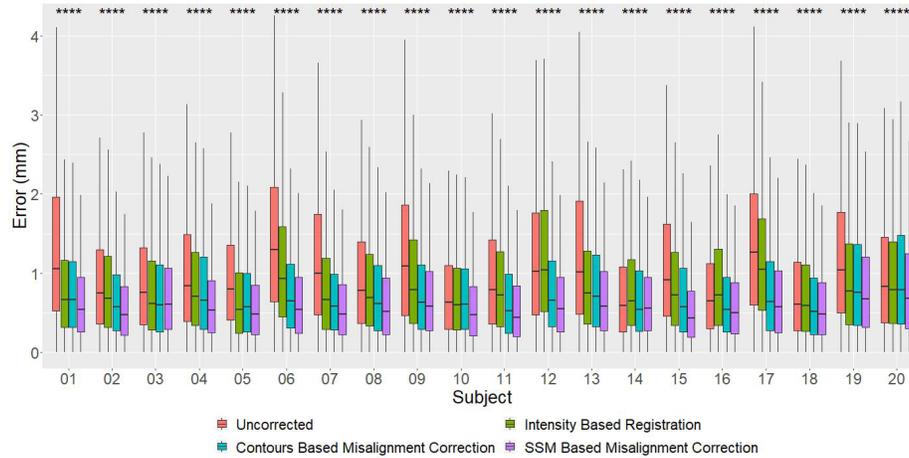


Fig. 4. Box-plots for the evaluation of misalignment correction. The ‘****’ symbol is used to indicate p-value of less than 0.0001.

and epicardial contours are measured as 0.52 ± 0.11 mm, 0.66 ± 0.06 mm, and 0.89 ± 0.19 mm, respectively, for 20 subjects. In few subjects where the contours based misalignment correction is already achieving the optimal performance (e.g. subjects 03 and 14), the SSM based misalignment correction attains the similar performance, but with less standard deviation.

5 Conclusion

The accurate patient-specific 3D modelling of heart meshes from 2D cine MR slices is important for several reasons. On one hand, it is useful for visualising heart structures and functions, including pathologies, on 3D heart shape for improved diagnosis and prediction of patient outcome. On the other hand, it is necessary in modelling and simulation-based applications, such as in-silico clinical trials. In this regard, our main contribution in this work is to develop a completely automated statistical shape model based approach for misalignment correction of 2D cine MR slices for accurate modelling of the biventricular heart meshes. Not only the proposed method can account for both in-plane and out-of-plane misalignments, it is applicable in the presence of only SAX slices as well as on both LAX and SAX slices. The performance of the proposed approach has been evaluated on a cohort of 20 subjects, randomly selected from the UK Biobank study. Our SSM based method has been able to reduce the misalignment between heart slices from average 1.14 ± 0.23 mm to average 0.72 ± 0.11 mm, and has presented statistically significant misalignment correction performance as compared to the intensity based as well as contours based misalignment correction approaches.

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